



SEQUENCE LISTING

<110> Meagher, Richard B.
Laterza, Vince

<120> RAPID PRODUCTION OF MONOCLONAL
ANTIBODIES

<130> 21099.0074U2

<140> 10/079,130
<141> 2002-02-20

<150> 60/270,322
<151> 2001-02-20

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 681
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 1
aagcttgc a ccatgccagg gggcttagaa gcccctcagag ccctgcctct cctcctcttc 60
ttgtcatacg cctgtttggg tcccgatgc caggccctgc gggtagaagg gggtccacca 120
tccctgacgg tgaacttggg cgaggaggcc cgccttcaccc tggaaaacaa tggcaggaac 180
cctaataatca catggtggtt cagccttcacg tctaaatca catggccccc agtgcactg 240
ggtcctggcc agggtaccac agggcagctg ttctccccg aagtaaacaa gaaccacagg 300
ggcttgtact ggtgccaagt gatagaaaaac aacatattaa aacgctcctg tggtacttac 360
ctccgcgtgc gcaatccagt ccctaggccc ttccctggaca tggggaaagg taccagaac 420
cgcacatcatca cagcagaagg gatcatctt cttgtgtgt cagtggtgcc agggacgctg 480
ctgttattca gaaacgggt gcaaaatgaa aagttgggg tggacatgcc agatgactat 540
gaagatgaaa atctctatga gggcctgaac cttgtatgact gttctatgtt tgaggacatc 600
tccaggggac tccaggggcac ctaccaggat gtggcaacc tccacattgg agatgcccag 660
ctggaaaagg catgagaatt c 681

<210> 2

<211> 705

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 2
aagcttgc a ccatggccac actgggtgtc tcttccatgc cctgccactg gctgttggtc 60
ctgctgctgc tcttctcagg tgagccggta ccagcaatga caagcagtga cctgccactg 120
aatttccaaag gaagcccttg ttcccgatgc tggcagcacc cgagggttgc agccaaaaag 180
cgagactcca tggtaagtt tcactgctac acaaaccact caggtgcact gacctgggtc 240
cgaaagcgag ggagccagca gccccaggaa ctggtctcag aagaggacg cattgtgcag 300
acccagaatg gctctgtcta caccctcact atccaaaaca tccagtagca ggataatgg 360
atctacttct gcaagcagaa atgtgacacgc gccaaccata atgtcaccga cagctgtggc 420

Attorney Docket No. 21099.0074U2

acggaaacttc tagtcttagg attcagcacg ttggaccaac tgaagcggcg	gaacacactg	480
aaagatggca ttatcttcat ccagaccctc ctcatcatcc tcttcatcat	tgtgcccata	540
ttcctgctac ttgacaagga tgacggcaag gctgggatcg aggaagatca	caccatgag	600
ggcttgaaca ttgaccagac agccacctat gaagacatag tgactctcg	gacaggggag	660
gtaaagtggc cggttaggaga gcatccaggc caggaatgac tcgag		705

<210> 3

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 3

Met Pro Gly Gly Leu Glu Ala Leu Arg Ala Leu Pro Leu Leu Leu Phe		
1 5 10 15		
Leu Ser Tyr Ala Cys Leu Gly Pro Gly Cys Gln Ala Leu Arg Val Glu		
20 25 30		
Gly Gly Pro Pro Ser Leu Thr Val Asn Leu Gly Glu Glu Ala Arg Leu		
35 40 45		
Thr Cys Glu Asn Asn Gly Arg Asn Pro Asn Ile Thr Trp Trp Phe Ser		
50 55 60		
Leu Gln Ser Asn Ile Thr Trp Pro Pro Val Pro Leu Gly Pro Gln		
65 70 75 80		
Gly Thr Thr Gly Gln Leu Phe Phe Pro Glu Val Asn Lys Asn His Arg		
85 90 95		
Gly Leu Tyr Trp Cys Gln Val Ile Glu Asn Asn Ile Leu Lys Arg Ser		
100 105 110		
Cys Gly Thr Tyr Leu Arg Val Arg Asn Pro Val Pro Arg Pro Phe Leu		
115 120 125		
Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala Glu Gly Ile		
130 135 140		
Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu Leu Phe Arg		
145 150 155 160		
Lys Arg Trp Gln Asn Glu Lys Phe Gly Val Asp Met Pro Asp Asp Tyr		
165 170 175		
Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn Leu Asp Asp Cys Ser Met		
180 185 190		
Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly Thr Tyr Gln Asp Val Gly		
195 200 205		
Asn Leu His Ile Gly Asp Ala Gln Leu Glu Lys Pro		
210 215 220		

<210> 4

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 4

Met Ala Thr Leu Val Leu Ser Ser Met Pro Cys His Trp Leu Leu Phe		
1 5 10 15		
Leu Leu Leu Leu Phe Ser Gly Glu Pro Val Pro Ala Met Thr Ser Ser		
20 25 30		

Attorney Docket No. 21099.0074U2

Asp Leu Pro Leu Asn Phe Gln Gly Ser Pro Cys Ser Gln Ile Trp Gln
35 40 45
His Pro Arg Phe Ala Ala Lys Lys Arg Ser Ser Met Val Lys Phe His
50 55 60
Cys Tyr Thr Asn His Ser Gly Ala Leu Thr Trp Phe Arg Lys Arg Gly
65 70 75 80
Ser Gln Gln Pro Gln Glu Leu Val Ser Glu Glu Gly Arg Ile Val Gln
85 90 95
Thr Gln Asn Gly Ser Val Tyr Thr Leu Thr Ile Gln Asn Ile Gln Tyr
100 105 110
Glu Asp Asn Gly Ile Tyr Phe Cys Lys Gln Lys Cys Asp Ser Ala Asn
115 120 125
His Asn Val Thr Asp Ser Cys Gly Thr Glu Leu Leu Val Leu Gly Phe
130 135 140
Ser Thr Leu Asp Gln Leu Lys Arg Arg Asn Thr Leu Lys Asp Gly Ile
145 150 155 160
Ile Leu Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile
165 170 175
Phe Leu Leu Leu Asp Lys Asp Asp Gly Lys Ala Gly Met Glu Glu Asp
180 185 190
His Thr Tyr Glu Gly Leu Asn Ile Asp Gln Thr Ala Thr Tyr Glu Asp
195 200 205
Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu His
210 215 220
Pro Gly Gln Glu
225